

SEQLIST_DAVI257.002APC.TXT

SEQUENCE LISTING

<110> Hart, Derek Nigel John
Kato, Masato

<120> DEC-205 (LY 75)/DCL-1 INTERGENIC SPLICE VARIANTS ASSOCIATED WITH
HODGKIN'S DISEASE, AND USES THEREOF

<130> DAVI257.002APC

<140> US 10/537,839

<141> 2005-06-06

<150> PCT/AU03/01634

<151> 2003-12-05

<150> AU2002953223

<151> 2002-12-06

<160> 32

<170> PatentIn version 3.1

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<211> 5622

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cct Pro	gtg Val	aca Thr	ttt Phe 900	gga Gly	gag Glu	gaa Glu	tgc Cys	ttg Leu 905	tac Tyr	atg Met	tct Ser	gcc Ala	aag Lys 910	act Thr	tgg Trp	2736
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ttt Phe 1475	gac Asp	tat Tyr	atc Ile	cca Pro	tgg Trp	aaa Lys 1480	ggc Gly	caa Gln	aca Thr	tct Ser	cct Pro 1485	gga Gly	aat Asn	tgt Cys	4464
gtt Val 1490	ctc Leu	ttg Leu	gat Asp	cca Pro	aaa Lys	gga Gly 1495	act Thr	tgg Trp	aaa Lys	cat His	gaa Glu 1500	aaa Lys	tgc Cys	aac Asn	4509
tct Ser 1505	gtt Val	aag Lys	gat Asp	ggt Gly	gct Ala	att Ile 1510	tgt Cys	tat Tyr	aaa Lys	cct Pro	aca Thr 1515	aaa Lys	tct Ser	aaa Lys	4554
aag Lys 1520	ctg Leu	tcc Ser	cgt Arg	ctt Leu	aca Thr	tat Tyr 1525	tca Ser	tca Ser	aga Arg	tgt Cys	cca Pro 1530	gca Ala	gca Ala	aaa Lys	4599
gag Glu 1535	aat Asn	ggg Gly	tca Ser	cgg Arg	tgg Trp	atc Ile 1540	cag Gln	tac Tyr	aag Lys	ggt Gly	cac His 1545	tgt Cys	tac Tyr	aag Lys	4644
tct Ser 1550	gat Asp	cag Gln	gca Ala	ttg Leu	cac His	agt Ser 1555	ttt Phe	tca Ser	gag Glu	gcc Ala	aaa Lys 1560	aaa Lys	ttg Leu	tgt Cys	4689

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tca Ser	aaa Lys 1565	cat His	gat Asp	cac His	tct Ser	gca Ala 1570	act Thr	atc Ile	gtt Val	tcc Ser	ata Ile 1575	aaa Lys	gat Asp	gaa Glu	4734
gat Asp	gag Glu 1580	aat Asn	aaa Lys	ttt Phe	gtg Val	agc Ser 1585	aga Arg	ctg Leu	atg Met	agg Arg	gaa Glu 1590	aat Asn	aat Asn	aac Asn	4779
att Ile	acc Thr 1595	atg Met	aga Arg	gtt Val	tgg Trp	ctt Leu 1600	gga Gly	tta Leu	tct Ser	caa Gln	cat His 1605	tct Ser	gtt Val	gac Asp	4824
cag Gln	tct Ser 1610	tgg Trp	agt Ser	tgg Trp	tta Leu	gat Asp 1615	gga Gly	tca Ser	gaa Glu	gtg Val	aca Thr 1620	ttt Phe	gtc Val	aaa Lys	4869
tgg Trp	gaa Glu 1625	aat Asn	aaa Lys	agt Ser	aag Lys	agt Ser 1630	ggt Gly	gtt Val	gga Gly	aga Arg	tgt Cys 1635	agc Ser	atg Met	ttg Leu	4914
ata Ile	gct Ala 1640	tca Ser	aat Asn	gaa Glu	act Thr	tgg Trp 1645	aaa Lys	aaa Lys	gtt Val	gaa Glu	tgt Cys 1650	gaa Glu	cat His	ggt Gly	4959
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act Thr	tgg Trp 1670	att Ile	cag Gln	ttc Phe	caa Gln	gac Asp 1675	agt Ser	tgt Cys	tac Tyr	att Ile	ttt Phe 1680	ctc Leu	caa Gln	gaa Glu	5049
gcc Ala	atc Ile 1685	aaa Lys	gta Val	gaa Glu	agc Ser	ata Ile 1690	gag Glu	gat Asp	gtc Val	aga Arg	aat Asn 1695	cag Gln	tgt Cys	act Thr	5094
gac Asp	cat His 1700	gga Gly	gcg Ala	gac Asp	atg Met	ata Ile 1705	agc Ser	ata Ile	cat His	aat Asn	gaa Glu 1710	gaa Glu	gaa Glu	aat Asn	5139
gct Ala	ttt Phe 1715	ata Ile	ctg Leu	gat Asp	act Thr	ttg Leu 1720	aaa Lys	aag Lys	caa Gln	tgg Trp	aaa Lys 1725	ggc Gly	cca Pro	gat Asp	5184
gat Asp	atc Ile 1730	cta Leu	cta Leu	ggc Gly	atg Met	ttt Phe 1735	tat Tyr	gac Asp	aca Thr	gat Asp	gat Asp 1740	gcg Ala	agt Ser	ttc Phe	5229
aag Lys	tgg Trp 1745	ttt Phe	gat Asp	aat Asn	tca Ser	aat Asn 1750	atg Met	aca Thr	ttt Phe	gat Asp	aag Lys 1755	tgg Trp	aca Thr	gac Asp	5274
caa Gln	gat Asp 1760	gat Asp	gat Asp	gag Glu	gat Asp	tta Leu 1765	gtt Val	gac Asp	acc Thr	tgt Cys	gct Ala 1770	ttt Phe	ctg Leu	cac His	5319
atc Ile	aag Lys 1775	aca Thr	ggt Gly	gaa Glu	tgg Trp	aaa Lys 1780	aaa Lys	gga Gly	aat Asn	tgt Cys	gaa Glu 1785	gtt Val	tct Ser	tct Ser	5364
gtg Val	gaa Glu	gga Gly	aca Thr	cta Leu	tgc Cys	aaa Lys	aca Thr	gct Ala	atc Ile	cca Pro	tac Tyr	aaa Lys	agg Arg	aaa Lys	5409

SEQLIST_DAVI257.002APC.TXT															
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Tyr	Leu	Ser	Asp	Asn	His	Ile	Leu	Ile	Ser	Ala	Leu	Val	Ile	Ala	
	1805					1810					1815				
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Ser	Thr	Val	Ile	Leu	Thr	Val	Leu	Gly	Ala	Ile	Ile	Trp	Phe	Leu	
	1820					1825					1830				
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Tyr	Lys	Lys	His	Ser	Asp	Ser	Arg	Phe	Thr	Thr	Val	Phe	Ser	Thr	
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Ala	Pro	Gln	Ser	Pro	Tyr	Asn	Glu	Asp	Cys	Val	Leu	Val	Val	Gly	
	1850					1855					1860				
gaa	gaa	aat	gaa	tat	cct	gtt	caa	ttt	gac	taa					5622
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Asn	Asp	Pro	Phe	Thr	Ile	Val	His	Gly	Asn	Thr	Gly	Lys	Cys	Ile	Lys
		35				40						45			
Pro	Val	Tyr	Gly	Trp	Ile	Val	Ala	Asp	Asp	Cys	Asp	Glu	Thr	Glu	Asp
	50					55					60				
Lys	Leu	Trp	Lys	Trp	Val	Ser	Gln	His	Arg	Leu	Phe	His	Leu	His	Ser
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Gln	Lys	Cys	Leu	Gly	Leu	Asp	Ile	Thr	Lys	Ser	Val	Asn	Glu	Leu	Arg
			85						90					95	
Met	Phe	Ser	Cys	Asp	Ser	Ser	Ala	Met	Leu	Trp	Trp	Lys	Cys	Glu	His
			100					105					110		
His	Ser	Leu	Tyr	Gly	Ala	Ala	Arg	Tyr	Arg	Leu	Ala	Leu	Lys	Asp	Gly
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SEQLIST_DAVI257.002APC.TXT

His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
130 135 140

Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
145 150 155 160

Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
165 170 175

Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
180 185 190

Trp Cys Ala Thr Thr Leu Asn Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
195 200 205

Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
210 215 220

Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
225 230 235 240

Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser
245 250 255

Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile
260 265 270

Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly
275 280 285

Trp Glu Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro
290 295 300

Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met
305 310 315 320

Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
325 330 335

Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
340 345 350

Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
355 360 365

Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys
370 375 380

SEQLIST_DAVI257.002APC.TXT

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His
385 390 395 400

Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
405 410 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
420 425 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp
435 440 445

Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser
450 455 460

Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys
465 470 475 480

Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser
485 490 495

Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
500 505 510

Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
515 520 525

Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu
530 535 540

Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu
545 550 555 560

Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly
565 570 575

Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala
580 585 590

Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys
595 600 605

Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys
610 615 620

SEQLIST_DAVI257.002APC.TXT

Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp
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 Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys
 645 650 655
 Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
 660 665 670
 Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
 675 680 685
 Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln
 690 695 700
 Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro
 705 710 715 720
 Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr
 725 730 735
 Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys
 740 745 750
 Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe
 755 760 765
 Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr
 770 775 780
 Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr
 785 790 795 800
 Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu
 805 810 815
 Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn
 820 825 830
 Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala
 835 840 845
 Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala
 850 855 860

SEQLIST_DAVI257.002APC.TXT

Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp
 865 870 875 880

Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe
 885 890 895

Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp
 900 905 910

Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe
 915 920 925

Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp
 930 935 940

Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn
 945 950 955 960

Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala
 965 970 975

Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser
 980 985 990

Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala
 995 1000 1005

Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn
 1010 1015 1020

Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro
 1025 1030 1035

Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu
 1040 1045 1050

Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys
 1055 1060 1065

Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg
 1070 1075 1080

His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg
 1085 1090 1095

Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn
 1100 1105 1110

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Leu	Tyr	Lys	Ile	Ile	Pro	Lys	Thr	Leu	Thr	Trp	His	Ser	Ala	Lys
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Arg	Glu	Cys	Leu	Lys	Ser	Asn	Met	Gln	Leu	Val	Ser	Ile	Thr	Asp
	1130					1135					1140			
Pro	Tyr	Gln	Gln	Ala	Phe	Leu	Ser	Val	Gln	Ala	Leu	Leu	His	Asn
	1145					1150					1155			
Ser	Ser	Leu	Trp	Ile	Gly	Leu	Phe	Ser	Gln	Asp	Asp	Glu	Leu	Asn
	1160					1165					1170			
Phe	Gly	Trp	Ser	Asp	Gly	Lys	Arg	Leu	His	Phe	Ser	Arg	Trp	Ala
	1175					1180					1185			
Glu	Thr	Asn	Gly	Gln	Leu	Glu	Asp	Cys	Val	Val	Leu	Asp	Thr	Asp
	1190					1195					1200			
Gly	Phe	Trp	Lys	Thr	Val	Asp	Cys	Asn	Asp	Asn	Gln	Pro	Gly	Ala
	1205					1210					1215			
Ile	Cys	Tyr	Tyr	Ser	Gly	Asn	Glu	Thr	Glu	Lys	Glu	Val	Lys	Pro
	1220					1225					1230			
Val	Asp	Ser	Val	Lys	Cys	Pro	Ser	Pro	Val	Leu	Asn	Thr	Pro	Trp
	1235					1240					1245			
Ile	Pro	Phe	Gln	Asn	Cys	Cys	Tyr	Asn	Phe	Ile	Ile	Thr	Lys	Asn
	1250					1255					1260			
Arg	His	Met	Ala	Thr	Thr	Gln	Asp	Glu	Val	His	Thr	Lys	Cys	Gln
	1265					1270					1275			
Lys	Leu	Asn	Pro	Lys	Ser	His	Ile	Leu	Ser	Ile	Arg	Asp	Glu	Lys
	1280					1285					1290			
Glu	Asn	Asn	Phe	Val	Leu	Glu	Gln	Leu	Leu	Tyr	Phe	Asn	Tyr	Met
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Ala	Ser	Trp	Val	Met	Leu	Gly	Ile	Thr	Tyr	Arg	Asn	Asn	Ser	Leu
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SEQLIST_DAVI257.002APC.TXT

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Thr	Asp	Gly	Phe	Trp	Asp	Ile	Gln	Thr	Phe	Lys	Val	Ile	Glu	Glu
1355						1360					1365			
Ala	Val	Tyr	Phe	His	Gln	His	Ser	Ile	Leu	Ala	Cys	Lys	Ile	Glu
1370						1375					1380			
Met	Val	Asp	Tyr	Lys	Glu	Glu	His	Asn	Thr	Thr	Leu	Pro	Gln	Phe
1385						1390					1395			
Met	Pro	Tyr	Glu	Asp	Gly	Ile	Tyr	Ser	Val	Ile	Gln	Lys	Lys	Val
1400						1405					1410			
Thr	Trp	Tyr	Glu	Ala	Leu	Asn	Met	Cys	Ser	Gln	Ser	Gly	Gly	His
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Leu	Ala	Ser	Val	His	Asn	Gln	Asn	Gly	Gln	Leu	Phe	Leu	Glu	Asp
1430						1435					1440			
Ile	Val	Lys	Arg	Asp	Gly	Phe	Pro	Leu	Trp	Val	Gly	Leu	Ser	Ser
1445						1450					1455			
His	Asp	Gly	Ser	Glu	Ser	Ser	Phe	Glu	Trp	Ser	Asp	Gly	Ser	Thr
1460						1465					1470			
Phe	Asp	Tyr	Ile	Pro	Trp	Lys	Gly	Gln	Thr	Ser	Pro	Gly	Asn	Cys
1475						1480					1485			
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SEQLIST_DAVI257.002APC.TXT

Asp	Glu	Asn	Lys	Phe	Val	Ser	Arg	Leu	Met	Arg	Glu	Asn	Asn	Asn
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Ile	Thr	Met	Arg	Val	Trp	Leu	Gly	Leu	Ser	Gln	His	Ser	Val	Asp
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Gln	Ser	Trp	Ser	Trp	Leu	Asp	Gly	Ser	Glu	Val	Thr	Phe	Val	Lys
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Trp	Glu	Asn	Lys	Ser	Lys	Ser	Gly	Val	Gly	Arg	Cys	Ser	Met	Leu
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Thr	Trp	Ile	Gln	Phe	Gln	Asp	Ser	Cys	Tyr	Ile	Phe	Leu	Gln	Glu
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Ala	Ile	Lys	Val	Glu	Ser	Ile	Glu	Asp	Val	Arg	Asn	Gln	Cys	Thr
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Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile Ile Trp Phe Leu
 1820 1825 1830

Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr Val Phe Ser Thr
 1835 1840 1845

Ala Pro Gln Ser Pro Tyr Asn Glu Asp Cys Val Leu Val Val Gly
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Glu Glu Asn Glu Tyr Pro Val Gln Phe Asp
 1865 1870

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ggaaccagag ggtttcacga ccctaattgta cgcactcggg ggtgtgaacc ggatgtaaaa	3240
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gaagtttatc tttaacgaag agaagttgga gtctgcggtg tgtccgcgct tggggatctg	240
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gtc atg ccc cac gca gcg ctg tcc tcg ctc gtg ctg ctg agc ctc gcc	408
Met Pro His Ala Ala Leu Ser Ser Leu Val Leu Leu Ser Leu Ala	
1 5 10 15	
act gcc atc gtc gcc gac tgt cct tca tct acc tgg gtc cag ttc caa	456
Thr Ala Ile Val Ala Asp Cys Pro Ser Ser Thr Trp Val Gln Phe Gln	
20 25 30	
ggc agc tgt tat gct ttt ctt caa gta acc atc aat gtg gaa aac ata	504
Gly Ser Cys Tyr Ala Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile	
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Ile	His	Asn	Glu	Glu	Glu	Asn	Ala	Phe	Ile	Leu	Asp	Thr	Leu	Gln	Lys		
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Arg	Trp	Lys	Gly	Pro	Asp	Asp	Leu	Leu	Leu	Gly	Met	Phe	Tyr	Asp	Thr		
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gat	gat	gca	act	ttc	aag	tgg	tat	gat	cat	tca	aat	atg	aca	ttc	gac	696	
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Lys	Trp	Ala	Asp	Gln	Asp	Gly	Glu	Asp	Leu	Val	Asp	Thr	Cys	Gly	Phe		
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Leu	Tyr	Thr	Lys	Thr	Gly	Glu	Trp	Arg	Lys	Gly	Asp	Cys	Glu	Ile	Ser		
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Ser	Val	Glu	Gly	Thr	Leu	Cys	Lys	Ala	Ala	Ile	Pro	Tyr	Asp	Lys	Lys		
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tat	tta	tca	gat	aac	cac	att	tta	ata	tcg	act	ctg	gtg	atc	gct	agc	888	
Tyr	Leu	Ser	Asp	Asn	His	Ile	Leu	Ile	Ser	Thr	Leu	Val	Ile	Ala	Ser		
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aca	gta	act	ctg	gca	ggt	ttg	gga	gcg	atc	att	tgg	ttc	ctc	tat	aga	936	
Thr	Val	Thr	Leu	Ala	Val	Leu	Gly	Ala	Ile	Ile	Trp	Phe	Leu	Tyr	Arg		
				180					185					190			
aga	aac	gcg	cgc	tct	ggc	ttc	acc	tct	ttt	tca	cct	gca	cca	ctg	tca	984	
Arg	Asn	Ala	Arg	Ser	Gly	Phe	Thr	Ser	Phe	Ser	Pro	Ala	Pro	Leu	Ser		
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cct	tac	agt	gat	ggc	tgt	gcc	ctg	gta	ggt	gca	gaa	gaa	gat	gaa	tat	1032	
Pro	Tyr	Ser	Asp	Gly	Cys	Ala	Leu	Val	Val	Ala	Glu	Glu	Asp	Glu	Tyr		
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gct	ggt	cag	ctg	gac	taagagtttg	gtaatatcag	gccagcatat	tgartccatt								1087	
Ala	Val	Gln	Leu	Asp													
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Ala Ile Val Ala Asp Cys Pro Ser Ser Thr Trp Val Gln Phe Gln Gly
20 25 30

Ser Cys Tyr Ala Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu
35 40 45

Asp Val Arg Lys Gln Cys Thr Asp His Gly Ala Asp Met Val Ser Ile
50 55 60

His Asn Glu Glu Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg
65 70 75 80

Trp Lys Gly Pro Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp
85 90 95

Asp Ala Thr Phe Lys Trp Tyr Asp His Ser Asn Met Thr Phe Asp Lys
100 105 110

Trp Ala Asp Gln Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu
115 120 125

Tyr Thr Lys Thr Gly Glu Trp Arg Lys Gly Asp Cys Glu Ile Ser Ser
130 135 140

Val Glu Gly Thr Leu Cys Lys Ala Ala Ile Pro Tyr Asp Lys Lys Tyr
145 150 155 160

Leu Ser Asp Asn His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr
165 170 175

Val Thr Leu Ala Val Leu Gly Ala Ile Ile Trp Phe Leu Tyr Arg Arg
180 185 190

Asn Ala Arg Ser Gly Phe Thr Ser Phe Ser Pro Ala Pro Leu Ser Pro
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Tyr Ser Asp Gly Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ala
210 215 220

Val Gln Leu Asp
225

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<212> DNA
<213> mammalian

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cttcaaatag aaattgcttc tcttcaacct cagacgccac acaggcgcgga acccctagac	240
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gactcgaccc tcgacgcgtg ggctgttcgt ggcggggggcc gggcgagagc cgcggcgcggt	360
cagtacgggg tgcgtcgcgga caggagcgag cagcagcact cggagcggtg acggtagcag	420
cggctgacag gaagtagatg gacccaggtc aaggttccgt cgacaatacg aaaagaagtt	480
cattggtagt tacacctttt gtatctccta cagtcttttg tcacgtgact ggtgccccgt	540
ctgtaccatt cgtatgtgtt acttctcctt ttgcgcaaat atgacctgtg aaacgttttc	600
gctaccttcc caggtctact agaggacgat ccgtacaaga tactgtgact actacgttga	660
aagttcacca tactagtaag ttatactgtt aagctgttca cccgtctagt tctaccactc	720
ctggatcaac tatggacacc aaaagacatg tggttctgtc cacttacctc ttttccccta	780
acactttaga gaagacacct cccttgtgaa acgtttcgtc gttaggggat actgttcttc	840
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agaaaaagtg gacgtggtga cagtggaatg tcactaccga cacgggacca tcaacgtctt	1020
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<210> 10
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 <222> (1)..(672)

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 <222> (5)..(5)
 <223> Xaa = Leu

<220>
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 <222> (13)..(13)
 <223> Xaa = Val, Ala

<220>
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 <222> (142)..(142)
 <223> Xaa = Thr

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gac tgt cct tcg tcc atc tgg gtt cag ttc caa ggc agc tgt tac act 96
Asp Cys Pro Ser Ser Ile Trp Val Gln Phe Gln Gly Ser Cys Tyr Thr
20 25 30

ttt ctt caa gta acc atc aat gtg gaa aac ata gag gat gtc aga aag 144
Phe Leu Gln Val Thr Ile Asn Val Glu Asn Ile Glu Asp Val Arg Lys
35 40 45

cag tgt act gat cac ggg gca gac ctg gta agt ata cac aat gaa gaa 192
Gln Cys Thr Asp His Gly Ala Asp Leu Val Ser Ile His Asn Glu Glu
50 55 60

gaa aac gca ttt ata ctg gac act tta caa aag cga tgg aaa ggc ccg 240
Glu Asn Ala Phe Ile Leu Asp Thr Leu Gln Lys Arg Trp Lys Gly Pro
65 70 75 80

gat gat ctt ctg cta ggc atg ttt tat gac act gat gat gca agt ttc 288
Asp Asp Leu Leu Leu Gly Met Phe Tyr Asp Thr Asp Asp Ala Ser Phe
85 90 95

aag tgg ttt gat cag tca aat atg aca ttc gac aag tgg gca gat gag 336
Lys Trp Phe Asp Gln Ser Asn Met Thr Phe Asp Lys Trp Ala Asp Glu
100 105 110

gat ggt gag gac cta gtt gac acc tgt ggt ttt ctg tat gcc aag aca 384
Asp Gly Glu Asp Leu Val Asp Thr Cys Gly Phe Leu Tyr Ala Lys Thr
115 120 125

ggt gaa tgg aga aaa gga aat tgt gaa atg tct tct gtg acr gga aca 432
Gly Glu Trp Arg Lys Gly Asn Cys Glu Met Ser Ser Val Xaa Gly Thr
130 135 140

ctt tgc aaa aca gca atc cca tat gac aag aag tat tta tca gat aac 480
Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn
145 150 155 160

cac att tta ata tcg act ctg gtg atc gct agc aca gtg act ctg gca 528
His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala
165 170 175

gtt ttg gga gcg gtc att tgg ttc ctc tat aga agg agc gca cgc tct 576
Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser
180 185 190

ggc ttc acc tct ttc tct cct gca cca caa tca cct tac agt gat ggc 624
Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly
195 200 205

tgt gct ctg gta gtt gcg gaa gaa gat gaa tac tct gtt cag ctg gac 672
Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp
210 215 220

tgagagtttg ggaacatcag acgagcacac tgaacacctt gacaagaaat aatttcctat 732
gcaagattgt catgtaaaat ttgccacgga aaactgaacc ttttatggta ttccttattc 792
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 <222> (5)..(5)
 <223> Xaa = Leu

<220>
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 <222> (13)..(13)
 <223> Xaa = Ala or Val

<220>
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 <222> (142)..(142)
 <223> Xaa = Thr

<400> 11

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Phe	Leu	Gln	Val	Thr	Ile	Asn	Val	Glu	Asn	Ile	Glu	Asp	Val	Arg	Lys
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Gln	Cys	Thr	Asp	His	Gly	Ala	Asp	Leu	Val	Ser	Ile	His	Asn	Glu	Glu
	50					55					60				

Glu	Asn	Ala	Phe	Ile	Leu	Asp	Thr	Leu	Gln	Lys	Arg	Trp	Lys	Gly	Pro
65					70					75					80

Asp	Asp	Leu	Leu	Leu	Gly	Met	Phe	Tyr	Asp	Thr	Asp	Asp	Ala	Ser	Phe
				85					90					95	

Lys	Trp	Phe	Asp	Gln	Ser	Asn	Met	Thr	Phe	Asp	Lys	Trp	Ala	Asp	Glu
			100					105					110		

Asp	Gly	Glu	Asp	Leu	Val	Asp	Thr	Cys	Gly	Phe	Leu	Tyr	Ala	Lys	Thr
		115					120					125			

Gly	Glu	Trp	Arg	Lys	Gly	Asn	Cys	Glu	Met	Ser	Ser	Val	Xaa	Gly	Thr
	130					135					140				

SEQLIST_DAVI257.002APC.TXT

Leu Cys Lys Thr Ala Ile Pro Tyr Asp Lys Lys Tyr Leu Ser Asp Asn
145 150 155 160

His Ile Leu Ile Ser Thr Leu Val Ile Ala Ser Thr Val Thr Leu Ala
165 170 175

Val Leu Gly Ala Val Ile Trp Phe Leu Tyr Arg Arg Ser Ala Arg Ser
180 185 190

Gly Phe Thr Ser Phe Ser Pro Ala Pro Gln Ser Pro Tyr Ser Asp Gly
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Cys Ala Leu Val Val Ala Glu Glu Asp Glu Tyr Ser Val Gln Leu Asp
210 215 220

<210> 12
<211> 979
<212> DNA
<213> mammalian

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gtgttacttc ttcttttgcg taaatatgac ctgtgaaatg ttttcgctac ctttccgggc 240
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gtcagtttat actgtaagct gttcaccgct ctactcctac cactcctgga tcaactgtgg 360
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cactgycctt gtgaaacggt ttgtcgtag ggtatactgt tcttcataaa tagtctattg 480
gtgtaaaatt atagctgaga ccactagcga tcgtgtcact gagaccgtca aaaccctcgc 540
cagtaaacca aggagatata ttcctcgcgt gcgagaccga agtggagaaa gagaggacgt 600
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caagtcgacc tgactctcaa acccttgtag tctgctcgtg tgacttgtgg aactgttctt 720
tattaaagga tacgttctaa cagtacattt taaacggtgc cttttgactt ggaaaatacc 780
ataaggaata agaagattgt tataaaagta cataagttac actgttttgt atttgggaaga 840
ctaattttcc tttttttcat ccaaagtctt ttccttgatc gtgtctcgat tgaatgtcca 900
aaagaattca tcaaaagtaa actcatttac tttcgatgtc atgttatttc gaccattttg 960
cgttttttt tttttttt 979

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 cacagttttt tcagctgcac accaatcacc ttataatgat gactgtgttt tagtagttgc 300
 agaggaaaac gaatatgata ttcaatttaa ctaagatttt ggaaatatca gactaagaca 360
 aatacctttc agtgattcct ctgtaagatt tcaatataaa acctgataat gaaaattagt 420
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 1 5

<210> 16
 <211> 42
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<213> mammalian

<220>

<221> CDS

<222> (1)..(42)

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42

<210> 17

<211> 14

<212> PRT

<213> mammalian

<400> 17

Lys Val Pro Leu Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
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<210> 18

<211> 42

<212> DNA

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<220>

<221> CDS

<222> (1)..(42)

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42

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<212> PRT

<213> mammalian

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Ala Ala Val Ala Asp Cys Pro Ser Ser Thr Trp Ile Gln Phe
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<210> 20

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<212> DNA

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ctg ctc ttc tgg ttc ttc gat ctc gcg gag ccc tct ggc cgc gca gct      96
Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala
20 25 30

aat gac ccc ttc acc atc gtc cat gga aat acg ggc aag tgc atc aag      144
Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
35 40 45

cca gtg tat ggc tgg ata gta gca gac gac tgt gat gaa act gag gac      192
Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
50 55 60

aag tta tgg aag tgg gtg tcc cag cat cgg ctc ttt cat ttg cac tcc      240
Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser
65 70 75 80

caa aag tgc ctt ggc ctc gat att acc aaa tcg gta aat gag ctg aga      288
Gln Lys Cys Leu Gly Leu Asp Ile Thr Lys Ser Val Asn Glu Leu Arg
85 90 95

atg ttc agc tgt gac tcc agt gcc atg ctg tgg tgg aaa tgt gag cac      336
Met Phe Ser Cys Asp Ser Ser Ala Met Leu Trp Trp Lys Cys Glu His
100 105 110

cac tct ctg tac gga gct gcc cgg tac cgg ctg gct ctg aag gat gga      384
His Ser Leu Tyr Gly Ala Ala Arg Tyr Arg Leu Ala Leu Lys Asp Gly
115 120 125

cat ggc aca gca atc tca aat gca tct gat gtc tgg aag aaa gga ggc      432
His Gly Thr Ala Ile Ser Asn Ala Ser Asp Val Trp Lys Lys Gly Gly
130 135 140

tca gag gaa agc ctt tgt gac cag cct tat cat gag atc tat acc aga      480
Ser Glu Glu Ser Leu Cys Asp Gln Pro Tyr His Glu Ile Tyr Thr Arg
145 150 155 160

gat ggg aac tct tat ggg aga cct tgt gaa ttt cca ttc tta att gat      528
Asp Gly Asn Ser Tyr Gly Arg Pro Cys Glu Phe Pro Phe Leu Ile Asp
165 170 175

ggg acc tgg cat cat gat tgc att ctt gat gaa gat cat agt ggg cca      576
Gly Thr Trp His His Asp Cys Ile Leu Asp Glu Asp His Ser Gly Pro
180 185 190

tgg tgt gcc acc acc tta aat tat gaa tat gac cga aag tgg ggc atc      624
Trp Cys Ala Thr Thr Leu Asn Tyr Tyr Glu Tyr Asp Arg Lys Trp Gly Ile
195 200 205

tgc tta aag cct gaa aac ggt tgt gaa gat aat tgg gaa aag aac gag      672
Cys Leu Lys Pro Glu Asn Gly Cys Glu Asp Asn Trp Glu Lys Asn Glu
210 215 220

cag ttt gga agt tgc tac caa ttt aat act cag acg gct ctt tct tgg      720
Gln Phe Gly Ser Cys Tyr Gln Phe Asn Thr Gln Thr Ala Leu Ser Trp
225 230 235

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aaa gaa gct tat gtt tca tgt cag aat caa gga gct gat tta ctg agc Lys Glu Ala Tyr Val Ser Cys Gln Asn Gln Gly Ala Asp Leu Leu Ser	768
atc aac agt gct gct gaa tta act tac ctt aaa gaa aaa gaa ggc att Ile Asn Ser Ala Ala Glu Leu Thr Tyr Leu Lys Glu Lys Glu Gly Ile	816
gct aag att ttc tgg att ggt tta aat cag cta tac tct gct aga ggc Ala Lys Ile Phe Trp Ile Gly Leu Asn Gln Leu Tyr Ser Ala Arg Gly	864
tgg gaa tgg tca gac cac aaa cca tta aac ttt ctc aac tgg gat cca Trp Trp Ser Asp His Lys Pro Leu Asn Phe Leu Asn Trp Asp Pro	912
gac agg ccc agt gca cct act ata ggt ggc tcc agc tgt gca aga atg Asp Arg Pro Ser Ala Pro Thr Ile Gly Gly Ser Ser Cys Ala Arg Met	960
gat gct gag tct ggt ctg tgg cag agc ttt tcc tgt gaa gct caa ctg Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu	1008
ccc tat gtc tgc agg aaa cca tta aat aat aca gtg gag tta aca gat Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp	1056
gtc tgg aca tac tca gat acc cgc tgt gat gca ggc tgg ctg cca aat Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn	1104
aat gga ttt tgc tat ctg ctg gta aat gaa agt aat tcc tgg gat aag Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys	1152
gca cat gcg aaa tgc aaa gcc ttc agt agt gac cta atc agc att cat Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His	1200
tct cta gca gat gtg gag gtg gtt gtc aca aaa ctc cat aat gag gat Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp	1248
atc aaa gaa gaa gtg tgg ata ggc ctt aag aac ata aac ata cca act Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr	1296
tta ttt cag tgg tca gat ggt act gaa gtt act cta aca tat tgg gat Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp	1344
gag aat gag cca aat gtt ccc tac aat aag acg ccc aac tgt gtt tcc Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser	1392
tac tta gga gag cta ggt cag tgg aaa gtc caa tca tgt gag gag aaa Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys	1440
cta aaa tat gta tgc aag aga aag gga gaa aaa ctg aat gac gca agt Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser	1488

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tct gat aag atg tgt cct cca gat gag ggc tgg aag aga cat gga gaa	1536
Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu	
500 505 510	
acc tgt tac aag att tat gag gat gag gtc cct ttt gga aca aac tgc	1584
Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys	
515 520 525	
aat ctg act atc act agc aga ttt gag caa gaa tac cta aat gat ttg	1632
Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu	
530 535 540	
atg aaa aag tat gat aaa tct cta aga aaa tac ttc tgg act ggc ctg	1680
Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu	
545 550 555 560	
aga gat gta gat tct tgt gga gag tat aac tgg gca act gtt ggt gga	1728
Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly	
565 570 575	
aga agg cgg gct gta acc ttt tcc aac tgg aat ttt ctt gag cca gct	1776
Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala	
580 585 590	
tcc ccg ggc ggc tgc gtg gct atg tct act gga aag tct gtt gga aag	1824
Ser Pro Gly Gly Cys Val Ala Met Ser Thr Gly Lys Ser Val Gly Lys	
595 600 605	
tgg gag gtg aag gac tgc aga agc ttc aaa gca ctt tca att tgc aag	1872
Trp Glu Val Lys Asp Cys Arg Ser Phe Lys Ala Leu Ser Ile Cys Lys	
610 615 620	
aaa atg agt gga ccc ctt ggg cct gaa gaa gca tcc cct aag cct gat	1920
Lys Met Ser Gly Pro Leu Gly Pro Glu Glu Ala Ser Pro Lys Pro Asp	
625 630 635 640	
gac ccc tgt cct gaa ggc tgg cag agt ttc ccc gca agt ctt tct tgt	1968
Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys	
645 650 655	
tat aag gta ttc cat gca gaa aga att gta aga aag agg aac tgg gaa	2016
Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu	
660 665 670	
gaa gct gaa cga ttc tgc caa gcc ctt gga gca cac ctt tct agc ttc	2064
Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe	
675 680 685	
agc cat gtg gat gaa ata aag gaa ttt ctt cac ttt tta acg gac cag	2112
Ser His Val Asp Glu Ile Lys Glu Phe Leu His Phe Leu Thr Asp Gln	
690 695 700	
ttc agt ggc cag cat tgg ctg tgg att ggt ttg aat aaa agg agc cca	2160
Phe Ser Gly Gln His Trp Leu Trp Ile Gly Leu Asn Lys Arg Ser Pro	
705 710 715 720	
gat tta caa gga tcc tgg caa tgg agt gat cgt aca cca gtg tct act	2208
Asp Leu Gln Gly Ser Trp Gln Trp Ser Asp Arg Thr Pro Val Ser Thr	
725 730 735	

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att atc atg cca aat gag ttt cag cag gat tat gac atc aga gac tgt Ile Ile Met Pro Asn Glu Phe Gln Gln Asp Tyr Asp Ile Arg Asp Cys 740 745 750	2256
gct gct gtc aag gta ttt cat agg cca tgg cga aga ggc tgg cat ttc Ala Ala Val Lys Val Phe His Arg Pro Trp Arg Arg Gly Trp His Phe 755 760 765	2304
tat gat gat aga gaa ttt att tat ttg agg cct ttt gct tgt gat aca Tyr Asp Asp Arg Glu Phe Ile Tyr Leu Arg Pro Phe Ala Cys Asp Thr 770 775 780	2352
aaa ctt gaa tgg gtg tgc caa att cca aaa ggc cgt act cca aaa aca Lys Leu Glu Trp Val Cys Gln Ile Pro Lys Gly Arg Thr Pro Lys Thr 785 790 800	2400
cca gac tgg tac aat cca gac cgt gct gga att cat gga cct cca ctt Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu 805 810 815	2448
ata att gaa gga agt gaa tat tgg ttt gtt gct gat ctt cac cta aac Ile Ile Glu Gly Ser Glu Tyr Trp Phe Val Ala Asp Leu His Leu Asn 820 825 830	2496
tat gaa gaa gcc gtc ctg tac tgt gcc agc aat cac agc ttt ctt gcg Tyr Glu Glu Ala Val Leu Tyr Cys Ala Ser Asn His Ser Phe Leu Ala 835 840 845	2544
act ata aca tct ttt gtg gga cta aaa gcc atc aaa aac aaa ata gca Thr Ile Thr Ser Phe Val Gly Leu Lys Ala Ile Lys Asn Lys Ile Ala 850 855 860	2592
aat ata tct ggt gat gga cag aag tgg tgg ata aga att agc gag tgg Asn Ile Ser Gly Asp Gly Gln Lys Trp Trp Ile Arg Ile Ser Glu Trp 865 870 875 880	2640
cca ata gat gat cat ttt aca tac tca cga tat cca tgg cac cgc ttt Pro Ile Asp Asp His Phe Thr Tyr Ser Arg Tyr Pro Trp His Arg Phe 885 890 895	2688
cct gtg aca ttt gga gag gaa tgc ttg tac atg tct gcc aag act tgg Pro Val Thr Phe Gly Glu Glu Cys Leu Tyr Met Ser Ala Lys Thr Trp 900 905 910	2736
ctt atc gac tta ggt aaa cca aca gac tgt agt acc aag ttg ccc ttc Leu Ile Asp Leu Gly Lys Pro Thr Asp Cys Ser Thr Lys Leu Pro Phe 915 920 925	2784
atc tgt gaa aaa tat aat gtt tct tcg tta gag aaa tac agc cca gat Ile Cys Glu Lys Tyr Asn Val Ser Ser Leu Glu Lys Tyr Ser Pro Asp 930 935 940	2832
tct gca gct aaa gtg caa tgt tct gag caa tgg att cct ttt cag aat Ser Ala Ala Lys Val Gln Cys Ser Glu Gln Trp Ile Pro Phe Gln Asn 945 950 955 960	2880
aag tgt ttt cta aag atc aaa ccc gtg tct ctc aca ttt tct caa gca Lys Cys Phe Leu Lys Ile Lys Pro Val Ser Leu Thr Phe Ser Gln Ala 965 970 975	2928
agc gat acc tgt cac tcc tat ggt ggc acc ctt cct tca gtg ttg agc Ser Asp Thr Cys His Ser Tyr Gly Gly Thr Leu Pro Ser Val Leu Ser 980 985 990	2976

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cag att gaa caa gac ttt att aca tcc ttg ctt ccg gat atg gaa gct	3024
Gln Ile Glu Gln Asp Phe Ile Thr Ser Leu Leu Pro Asp Met Glu Ala	
995 1000 1005	
act tta tgg att ggt ttg cgc tgg act gcc tat gaa aag ata aac	3069
Thr Leu Trp Ile Gly Leu Arg Trp Thr Ala Tyr Glu Lys Ile Asn	
1010 1015 1020	
aaa tgg aca gat aac aga gag ctg acg tac agt aac ttt cac cca	3114
Lys Trp Thr Asp Asn Arg Glu Leu Thr Tyr Ser Asn Phe His Pro	
1025 1030 1035	
tta ttg gtt agt ggg agg ctg aga ata cca gaa aat ttt ttt gag	3159
Leu Leu Val Ser Gly Arg Leu Arg Ile Pro Glu Asn Phe Phe Glu	
1040 1045 1050	
gaa gag tct cgc tac cac tgt gcc cta ata ctc aac ctc caa aaa	3204
Glu Glu Ser Arg Tyr His Cys Ala Leu Ile Leu Asn Leu Gln Lys	
1055 1060 1065	
tca ccg ttt act ggg acg tgg aat ttt aca tcc tgc agt gaa cgc	3249
Ser Pro Phe Thr Gly Thr Trp Asn Phe Thr Ser Cys Ser Glu Arg	
1070 1075 1080	
cac ttt gtg tct ctc tgt cag aaa tat tca gaa gtt aaa agc aga	3294
His Phe Val Ser Leu Cys Gln Lys Tyr Ser Glu Val Lys Ser Arg	
1085 1090 1095	
cag acg ttg cag aat gct tca gaa act gta aag tat cta aat aat	3339
Gln Thr Leu Gln Asn Ala Ser Glu Thr Val Lys Tyr Leu Asn Asn	
1100 1105 1110	
ctg tac aaa ata atc cca aag act ctg act tgg cac agt gct aaa	3384
Leu Tyr Lys Ile Ile Pro Lys Thr Leu Thr Trp His Ser Ala Lys	
1115 1120 1125	
agg gag tgt ctg aaa agt aac atg cag ctg gtg agc atc acg gac	3429
Arg Glu Cys Leu Lys Ser Asn Met Gln Leu Val Ser Ile Thr Asp	
1130 1135 1140	
cct tac cag cag gca ttc ctc agt gtg cag gcg ctc ctt cac aac	3474
Pro Tyr Gln Gln Ala Phe Leu Ser Val Gln Ala Leu Leu His Asn	
1145 1150 1155	
tct tcc tta tgg atc gga ctc ttc agt caa gat gat gaa ctc aac	3519
Ser Ser Leu Trp Ile Gly Leu Phe Ser Gln Asp Asp Glu Leu Asn	
1160 1165 1170	
ttt ggt tgg tca gat ggg aaa cgt ctt cat ttt agt cgc tgg gct	3564
Phe Gly Trp Ser Asp Gly Lys Arg Leu His Phe Ser Arg Trp Ala	
1175 1180 1185	
gaa act aat ggg caa ctc gaa gac tgt gta gta tta gac act gat	3609
Glu Thr Asn Gly Gln Leu Glu Asp Cys Val Val Leu Asp Thr Asp	
1190 1195 1200	
gga ttc tgg aaa aca gtt gat tgc aat gac aat caa cca ggt gct	3654
Gly Phe Trp Lys Thr Val Asp Cys Asn Asp Asn Gln Pro Gly Ala	
1205 1210 1215	

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att tgc tac tat tca gga aat gag act gaa aaa gag gtc aaa cca Ile Cys Tyr Tyr Ser Gly Asn Glu Thr Glu Lys Glu Val Lys Pro	3699
1220 1225 1230	
ggt gac agt gtt aaa tgt cca tct cct gtt cta aat act ccg tgg Val Asp Ser Val Lys Cys Pro Ser Pro Val Leu Asn Thr Pro Trp	3744
1235 1240 1245	
ata cca ttt cag aac tgt tgc tac aat ttc ata ata aca aag aat Ile Pro Phe Gln Asn Cys Cys Tyr Asn Phe Ile Ile Thr Lys Asn	3789
1250 1255 1260	
agg cat atg gca aca aca cag gat gaa gtt cat act aaa tgc cag Arg His Met Ala Thr Thr Gln Asp Glu Val His Thr Lys Cys Gln	3834
1265 1270 1275	
aaa ctg aat cca aaa tca cat att ctg agt att cga gat gaa aag Lys Leu Asn Pro Lys Ser His Ile Leu Ser Ile Arg Asp Glu Lys	3879
1280 1285 1290	
gag aat aac ttt gtt ctt gag caa ctg ctg tac ttc aat tat atg Glu Asn Asn Phe Val Leu Glu Gln Leu Leu Tyr Phe Asn Tyr Met	3924
1295 1300 1305	
gct tca tgg gtc atg tta gga ata act tat aga aat aat tct ctt Ala Ser Trp Val Met Leu Gly Ile Thr Tyr Arg Asn Asn Ser Leu	3969
1310 1315 1320	
atg tgg ttt gat aag acc cca ctg tca tat aca cat tgg aga gca Met Trp Phe Asp Lys Thr Pro Leu Ser Tyr Thr His Trp Arg Ala	4014
1325 1330 1335	
gga aga cca act ata aaa aat gag aag ttt ttg gct ggt tta agt Gly Arg Pro Thr Ile Lys Asn Glu Lys Phe Leu Ala Gly Leu Ser	4059
1340 1345 1350	
act gac ggc ttc tgg gat att caa acc ttt aaa gtt att gaa gaa Thr Asp Gly Phe Trp Asp Ile Gln Thr Phe Lys Val Ile Glu Glu	4104
1355 1360 1365	
gca gtt tat ttt cac cag cac agc att ctt gct tgt aaa att gaa Ala Val Tyr Phe His Gln His Ser Ile Leu Ala Cys Lys Ile Glu	4149
1370 1375 1380	
atg gtt gac tac aaa gaa gaa cat aat act aca ctg cca cag ttt Met Val Asp Tyr Lys Glu Glu His Asn Thr Thr Leu Pro Gln Phe	4194
1385 1390 1395	
atg cca tat gaa gat ggt att tac agt gtt att caa aaa aag gta Met Pro Tyr Glu Asp Gly Ile Tyr Ser Val Ile Gln Lys Lys Val	4239
1400 1405 1410	
aca tgg tat gaa gca tta aac atg tgt tct caa agt gga ggt cac Thr Trp Tyr Glu Ala Leu Asn Met Cys Ser Gln Ser Gly Gly His	4284
1415 1420 1425	
ttg gca agc gtt cac aac caa aat ggc cag ctc ttt ctg gaa gat Leu Ala Ser Val His Asn Gln Asn Gly Gln Leu Phe Leu Glu Asp	4329
1430 1435 1440	
att gta aaa cgt gat gga ttt cca cta tgg gtt ggg ctc tca agt	4374

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Ile Val 1445	Lys Arg Asp Gly	Phe 1450	Pro Leu Trp Val Gly 1455	Leu Ser Ser	
cat gat 1460	gga agt gaa tca agt 1465	ttt gaa tgg tct gat 1470	ggt agt aca 4419		
His Asp 1460	Gly Ser Glu Ser	Phe Glu Trp Ser	Gly Ser Thr		
ttt gat 1475	tat atc cca tgg aaa 1480	ggc caa aca tct cct 1485	gga aat tgt 4464		
Phe Asp 1475	Tyr Ile Pro Trp	Gly Gln Thr Ser	Gly Asn Cys		
gtt ctc 1490	ttg gat cca aaa gga 1495	act tgg aaa cat gaa 1500	aaa tgc aac 4509		
Val Leu 1490	Leu Asp Pro Lys	Thr Trp Lys His	Lys Cys Asn		
tct gtt 1505	aag gat ggt gct att 1510	tgt tat aaa cct aca 1515	aaa tct aaa 4554		
Ser Val 1505	Lys Asp Gly Ala	Cys Tyr Lys Pro	Lys Ser Lys		
aag ctg 1520	tcc cgt ctt aca tat 1525	tca tca aga tgt cca 1530	gca gca aaa 4599		
Lys Leu 1520	Ser Arg Leu Thr	Ser Ser Arg Cys	Ala Ala Lys		
gag aat 1535	ggg tca cgg tgg atc 1540	cag tac aag ggt cac 1545	tgt tac aag 4644		
Glu Asn 1535	Gly Ser Arg Trp	Gln Tyr Lys Gly	Cys Tyr Lys		
tct gat 1550	cag gca ttg cac agt 1555	ttt tca gag gcc aaa 1560	aaa ttg tgt 4689		
Ser Asp 1550	Gln Ala Leu His	Phe Ser Glu Ala	Lys Leu Cys		
tca aaa 1565	cat gat cac tct gca 1570	act atc gtt tcc ata 1575	aaa gat gaa 4734		
Ser Lys 1565	His Asp His Ser	Thr Ile Val Ser	Lys Asp Glu		
gat gag 1580	aat aaa ttt gtg agc 1585	aga ctg atg agg gaa 1590	aat aat aac 4779		
Asp Glu 1580	Asn Lys Phe Val	Arg Leu Met Arg	Asn Asn Asn		
att acc 1595	atg aga gtt tgg ctt 1600	gga tta tct caa cat 1605	tct gtt gac 4824		
Ile Thr 1595	Met Arg Val Trp	Gly Leu Ser Gln	Ser Val Asp		
tgt cct 1610	tca tct act tgg att 1615	cag ttc caa gac agt 1620	tgt tac att 4869		
Cys Pro 1610	Ser Ser Thr Trp	Gln Phe Gln Asp	Cys Tyr Ile		
ttt ctc 1625	caa gaa gcc atc aaa 1630	gta gaa agc ata gag 1635	gat gtc aga 4914		
Phe Leu 1625	Gln Glu Ala Ile	Val Glu Ser Ile	Asp Val Arg		
aat cag 1640	tgt act gac cat gga 1645	gcg gac atg ata agc 1650	ata cat aat 4959		
Asn Gln 1640	Cys Thr Asp His	Ala Asp Met Ile	Ile His Asn		
gaa gaa 1655	gaa aat gct ttt ata 1660	ctg gat act ttg aaa 1665	aag caa tgg 5004		
Glu Glu 1655	Glu Asn Ala Phe	Leu Asp Thr Leu	Lys Gln Trp		
aaa ggc 1670	cca gat gat atc cta 1675	cta ggc atg ttt tat 1680	gac aca gat 5049		
Lys Gly 1670	Pro Asp Asp Ile	Leu Gly Met Phe	Asp Thr Asp		

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gat gcg agt ttc aag tgg ttt gat aat tca aat atg aca ttt gat	5094
Asp Ala Ser Phe Lys Trp Phe Asp Asn Ser Asn Met Thr Phe Asp	
1685 1690 1695	
aag tgg aca gac caa gat gat gat gag gat tta gtt gac acc tgt	5139
Lys Trp Thr Asp Gln Asp Asp Asp Glu Asp Leu Val Asp Thr Cys	
1700 1705 1710	
gct ttt ctg cac atc aag aca ggt gaa tgg aaa aaa gga aat tgt	5184
Ala Phe Leu His Ile Lys Thr Gly Glu Trp Lys Lys Gly Asn Cys	
1715 1720 1725	
gaa gtt tct tct gtg gaa gga aca cta tgc aaa aca gct atc cca	5229
Glu Val Ser Ser Val Glu Gly Thr Leu Cys Lys Thr Ala Ile Pro	
1730 1735 1740	
tac aaa agg aaa tat tta tca gat aac cac att tta ata tca gca	5274
Tyr Lys Arg Lys Tyr Leu Ser Asp Asn His Ile Leu Ile Ser Ala	
1745 1750 1755	
ttg gtg att gct agc acg gta att ttg aca gtt ttg gga gca atc	5319
Leu Val Ile Ala Ser Thr Val Ile Leu Thr Val Leu Gly Ala Ile	
1760 1765 1770	
att tgg ttc ctg tac aaa aaa cat tct gat tct cgt ttc acc aca	5364
Ile Trp Phe Leu Tyr Lys Lys His Ser Asp Ser Arg Phe Thr Thr	
1775 1780 1785	
gtt ttt tca acc gca ccc caa tca cct tat aat gaa gac tgt gtt	5409
Val Phe Ser Thr Ala Pro Gln Ser Pro Tyr Asn Glu Asp Cys Val	
1790 1795 1800	
ttg gta gtt gga gaa gaa aat gaa tat cct gtt caa ttt gac taa	5454
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1805 1810 1815	

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Leu Leu Phe Trp Phe Phe Asp Leu Ala Glu Pro Ser Gly Arg Ala Ala
 20 25 30

Asn Asp Pro Phe Thr Ile Val His Gly Asn Thr Gly Lys Cys Ile Lys
 35 40 45

Pro Val Tyr Gly Trp Ile Val Ala Asp Asp Cys Asp Glu Thr Glu Asp
 50 55 60

Lys Leu Trp Lys Trp Val Ser Gln His Arg Leu Phe His Leu His Ser

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Gln	Lys	Cys	Leu	Gly 85	Leu	Arg
					Thr	
					Lys 90	
					Ser	
					Val	
					Asn	
					Glu	
					Leu	
					Arg	
Met	Phe	Ser	Cys 100	Asp	Ser	
					Ser	
					Ala	
					Met 105	
					Leu	
					Trp	
					Trp	
					Lys	
					Cys 110	
					Glu	
					His	
His	Ser	Leu 115	Tyr	Gly	Ala	
					Ala	
					Arg 120	
					Tyr	
					Arg	
					Leu	
					Ala	
					Leu 125	
					Lys	
					Asp	
					Gly	
His	Gly 130	Thr	Ala	Ile	Ser	
					Asn 135	
					Ala	
					Ser	
					Asp	
					Val	
					Trp 140	
					Lys	
					Lys	
					Gly	
					Gly	
Ser	Glu	Glu	Ser	Leu	Cys 150	
					Asp	
					Gln	
					Pro	
					Tyr	
					His 155	
					Glu	
					Ile	
					Tyr	
					Thr	
					Arg 160	
Asp	Gly	Asn	Ser	Tyr 165	Gly	
					Arg	
					Pro	
					Cys	
					Glu 170	
					Phe	
					Pro	
					Phe	
					Leu	
					Ile 175	
					Asp	
Gly	Thr	Trp	His 180	His	Asp	
					Cys	
					Ile	
					Leu 185	
					Asp	
					Glu	
					Asp	
					His	
					Ser 190	
					Gly	
					Pro	
Trp	Cys	Ala 195	Thr	Thr	Leu	
					Asn	
					Tyr 200	
					Glu	
					Tyr	
					Asp	
					Arg	
					Lys 205	
					Trp	
					Gly	
					Ile	
Cys	Leu 210	Lys	Pro	Glu	Asn	
					Gly 215	
					Cys	
					Glu	
					Asp	
					Asn	
					Trp 220	
					Glu	
					Lys	
					Asn	
					Glu	
Gln	Phe	Gly	Ser	Cys	Tyr 230	
					Gln	
					Phe	
					Asn	
					Thr	
					Gln 235	
					Thr	
					Ala	
					Leu	
					Ser	
					Trp 240	
Lys	Glu	Ala	Tyr	Val 245	Ser	
					Cys	
					Gln	
					Asn	
					Gln 250	
					Gly	
					Ala	
					Asp	
					Leu	
					Leu 255	
					Ser	
Ile	Asn	Ser	Ala 260	Ala	Glu	
					Leu	
					Thr	
					Tyr 265	
					Leu	
					Lys	
					Glu	
					Lys	
					Glu 270	
					Gly	
					Ile	
Ala	Lys	Ile 275	Phe	Trp	Ile	
					Gly	
					Leu 280	
					Asn	
					Gln	
					Leu	
					Tyr	
					Ser 285	
					Ala	
					Arg	
					Gly	
Trp	Glu 290	Trp	Ser	Asp	His	
					Lys 295	
					Pro	
					Leu	
					Asn	
					Phe	
					Leu 300	
					Asn	
					Trp	
					Asp	
					Pro	
Asp	Arg	Pro	Ser	Ala	Pro 310	
					Thr	
					Ile	
					Gly	
					Gly	
					Ser 315	
					Ser	
					Cys	
					Ala	
					Arg	
					Met 320	

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Asp Ala Glu Ser Gly Leu Trp Gln Ser Phe Ser Cys Glu Ala Gln Leu
325 330 335

Pro Tyr Val Cys Arg Lys Pro Leu Asn Asn Thr Val Glu Leu Thr Asp
340 345 350

Val Trp Thr Tyr Ser Asp Thr Arg Cys Asp Ala Gly Trp Leu Pro Asn
355 360 365

Asn Gly Phe Cys Tyr Leu Leu Val Asn Glu Ser Asn Ser Trp Asp Lys
370 375 380

Ala His Ala Lys Cys Lys Ala Phe Ser Ser Asp Leu Ile Ser Ile His
385 390 395 400

Ser Leu Ala Asp Val Glu Val Val Val Thr Lys Leu His Asn Glu Asp
405 410 415

Ile Lys Glu Glu Val Trp Ile Gly Leu Lys Asn Ile Asn Ile Pro Thr
420 425 430

Leu Phe Gln Trp Ser Asp Gly Thr Glu Val Thr Leu Thr Tyr Trp Asp
435 440 445

Glu Asn Glu Pro Asn Val Pro Tyr Asn Lys Thr Pro Asn Cys Val Ser
450 455 460

Tyr Leu Gly Glu Leu Gly Gln Trp Lys Val Gln Ser Cys Glu Glu Lys
465 470 475 480

Leu Lys Tyr Val Cys Lys Arg Lys Gly Glu Lys Leu Asn Asp Ala Ser
485 490 495

Ser Asp Lys Met Cys Pro Pro Asp Glu Gly Trp Lys Arg His Gly Glu
500 505 510

Thr Cys Tyr Lys Ile Tyr Glu Asp Glu Val Pro Phe Gly Thr Asn Cys
515 520 525

Asn Leu Thr Ile Thr Ser Arg Phe Glu Gln Glu Tyr Leu Asn Asp Leu
530 535 540

Met Lys Lys Tyr Asp Lys Ser Leu Arg Lys Tyr Phe Trp Thr Gly Leu
545 550 555 560

Arg Asp Val Asp Ser Cys Gly Glu Tyr Asn Trp Ala Thr Val Gly Gly

565

570

575

Arg Arg Arg Ala Val Thr Phe Ser Asn Trp Asn Phe Leu Glu Pro Ala
580 585 590

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Asp Pro Cys Pro Glu Gly Trp Gln Ser Phe Pro Ala Ser Leu Ser Cys
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Tyr Lys Val Phe His Ala Glu Arg Ile Val Arg Lys Arg Asn Trp Glu
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Glu Ala Glu Arg Phe Cys Gln Ala Leu Gly Ala His Leu Ser Ser Phe
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Pro Asp Trp Tyr Asn Pro Asp Arg Ala Gly Ile His Gly Pro Pro Leu
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